> 0 < 0 | O IntelliGenetics > 0 < 0 |

GENALIGN - Multiple Sequence Alignment Program Release 5.4

Wed 12 Jan 105 12:57:02-PST Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off

MAINO-Res-length = 2 DELetion-weight = 5.00 LEngth-factor = 0 MAtching-weight = 1.00 NUCLEIC-Res-length = 4 Spread-factor = 50

Amino acids 1-1531 (MDR)
= SEQ ID NO:4 OF 5,766,880
(For example)
of A AWS7486
1532-1537 = 6 GHCIME Space

Clustered order of selected sequences:

8. US-10-665-283-8 (1-1947) 1, US-10-665-283-1 (1-1927) 6. US-10-665-283-6 (1-1927) 4. US-10-665-283-4 (1-1891) Region Alignment: (listed in Clustered order)

LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL MALRGFCSADGSDPLWDWNVTWNTSNPDFTXCFQNTVLVWVPCFYLWACFPFYFLXLSRHD rgyiqmtplnktktalgfllwivcwadlfysfwersrgiflapvflvsptllgittllatf LIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLL IQLVLSCFSDRSPLFSETIHDPNPCPESSASFLSRITFWWITGLIVRGYRQPLEGSDLWS 62 RGYIQMTPIANTIKTALGFILMIVCWADLFYSFWERSRGFFIAPVFLVSFULGFT 184 I 123 123 62 123 184 184 62 62 123 consensus US-10-665-US-10-665-US-10-665-US-10-665-US-10-665consensus consensus US-10-665-US-10-665-US-10-665-US-10-665-US-10-665-US-10-665-US-10-665-US-10-665-Searth Mokes

184 IQLVLSCFSDRSPLFSETIHDPNPCPESSASFLSRITFWWITGLIVRGYRQPLEGSDLWSL IQLVLSCFSDRSPLFSETIHDPNPCPESSASFLSRITFWWITGLIVRGYRQPLEGSDLWSL	245 NKEDTSEQVVPULVKNWKKECAKTRKOPVKVVYSSKDPAQPKESSKVDANEEVEALIUKSP 245 NKEDTSEQVVPULVKOWKKECAKTRKOPVKVVYSSKDPAQPKESSKVDANEEVEALIUKSP 245 NKEDTSEQVVPULVKOWKKECAKTRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIUKSP 246 NKEDTSEQVVPULVKOWKKECAKTRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIUKSP 247 NKEDTSEQVVPULVKOWKKECAKTRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIUKSP NKEDTSEQVVPULVKOWKKECAKTRKQPVKVVYSSKDPAQPKESSKVDANEEVEALIUKSP	306 OKEWNPSLEKULYKTPGPYFLMSFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWGGYFY 306 OKEWNPSLEKULYKTFGPYFLMSFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWGGYFY 306 OKEWNPSLEKULYKTFGPYFLMSFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWGGYFY 306 OKEWNPSLEKULYKTFGPYFLMSFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWGGYFY 306 OKEWNPSLEKULYKTFGPYFLMSFFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWGGYFY OKEWNPSLFKVLYKTFGPYFLMSFFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWGGYFY	367 TVLLFVTACLQTLVLHQYPHICFVSGMRIKTAVIGAVYRKALVITNSARKSSTVGEIVNLM	428 SVDAQREMDLATYINMIWSAPLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTK	489 TYQVAHMKSKDNRIKLANBILINGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVG	550 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPPVISSIVQAS 550 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPVISSIVQAS 550 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPWVISSIVQAS 550 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPWVISSIVQAS 550 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPWVISSIVQAS 550 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPWVISSIVQAS 750 TFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFPLNILPWVISSIVQAS	611 VSLKRLRIFLSHEELEPDSIERRPVKDGGGTNSITVRNATFTWARSDPFTLNGITFSIPEG
US-10-665- consensus	US-10-665- US-10-665- US-10-665- US-10-665-	US-10-665- US-10-665- US-10-665- CONSENBUB	US-10-665- US-10-665- US-10-665- US-10-665-	US-10-665- US-10-665- US-10-665- US-10-665-	US-10-665- US-10-665- US-10-665- US-10-665-	US-10-665- US-10-665- US-10-665- US-10-665-	US-10-665-

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B 1282 - 1282 - 1282 - 1282 - 1283 - 1343 - 1343 - 1404 - 1404	
1282	
- 1282 - 1282 - 1282	
- 1221 - 1221 8	
- 1221 - 1221	
<u> </u>	794 PLSAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQE
US-10-665- 1160 LGVS US-10-665- 1160 LGVS	733 EEPYYRSVIQACALLEPDLEILPSGDRTEIGEKGVNLSGGGQQQQRVSLASLAVYSNADIYLFDD EEPYYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQQQQRVSLARAVYSNADIYLFDD
- 1160	733 EEPYYKSVIQACALLPDLEILESGBRTSIGEKGVNLSGGCKOKVSLAKAYSKNAII ILPID 733 EEPYYKSVIQACALLPDLEILESGBRTSIGEKGVNLSGGCKOKVSLAKAVSKNADIYLPDD 734 EEPYYRSVIQACALLPDLEILESGBRTSIGEKGVNLSGGCKOKVSLAKAVSKNADIYLPDD 735 EEPYYRSVIQACALLPDLEILESGBRTSIGEKGVNLSGGCKOKVSLAKAVSKNADIYLPDD 736 EEPYYRSVIQACALLPDLEILESGBRTSIGEKGVNLSGGCKOKVSLAKAVSKNADIYLPDD 737 EFYYRSVIQACALLPDLEILESGBRTSIGEKGVNLSGGCOKOKVSLAKAVSKNADIYLPDD
US-10-665- 1099 FNVI 	ALVAVVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQL
1099	672 ALVAVVGQVGCGKSSLLSALLAEMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQL
US-10-665- 1099 FNVI	
CONSENSUS SIGG	672 ALVAVVGQVGCGKSSLLSALLAEMDKYEGHVATKGSVAYVPQQANIQNDSLRSNILFGCQL
US-10-665- 1038 SIGG	
US-10-665- 1038 SIGG	VSLKRLRIFLSHEELEPDSIERRPVKDGGGTNSITVRNATFTWARSDPPTLNGITFSIPEG
- 1038	bil vslkkelritelsheebevslerktvkloggivel i vkarifiwaksdifiritelsifes
019 0101 .333.01.2m	

- 1038 SIGGILASRCLHVU 	5- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL 5- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL 5- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL 5- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL 6- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL 7- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL 8- 1099 FNVIGACIVILLATPIAAIIIPPLGLIYFFVQRPYVASSRQLKRLESVSRSPVYSHFNETL		5- 1221 SRHSLSAGLVGLSVSSLQVTTYLAMLVRMSSEMETNIVAVERLKEYSETEKEAPWQIQET	- 1282 A - 1282 A - 1282 A - 1282 A - 1282 A	- 1343 I - 1343 I - 1343 I - 1343 I	
US-10-665 US-10-665 US-10-665 US-10-665	US-10-665 US-10-665 US-10-665 US-10-665	US-10-665 US-10-665 US-10-665 US-10-665	US-10-665 US-10-665 US-10-665 US-10-665	US-10-665 US-10-665 US-10-665 US-10-665	US-10-665 US-10-665 US-10-665 US-10-665	US-10-665 US-10-665 US-10-665

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US-10-665- consensus	1404	
US-10-665- US-10-665- US-10-665- CONSENBUS	1465 1465 1465 1465	DDLIQSTIRTQFEDCTVLTIAHRLNTIMDYTRVIVLDXGEIQEYGABSDLLQQRGLFYSMA
US-10-665- US-10-665- US-10-665- US-10-665-	1526 1526 1526 1526	KDAGLVGCGGGMLSRKGI I PEBYVLTRLAEDPAEPRYRTRERRARFVSKKGNCNVAHKNI KDAGLVGCGGGMLSRKGI I PEBYVLTRLAEDPAEPRYRTRERRARFVSKKGNCNVAHKNI KDAGLVGGGGGMLSRKGI I PEBYVLTRLAEDPAEPRYRTRERRARFVSKKGNCNVAHKNI KDAGLVGGGGGGMLSRKGI I PEBYVLTRLAEDPAEPRYRTRERRARFVSKKGNCNVAHKNI KDAGLVGGGGGMLSRKGI I PEBYVLTRLAEDPAEPRYRTRERRARFVSKKGNCNVAHKNI KDAGLVGGGGGMLSRKGI I PEBYVLTRLAEDPAEPRYRTRERRARFVSKKGNCNVAHKNI
US-10-665- US-10-665- US-10-665- US-10-665- CORBERBUB	1587 1587 1587 1587	REGGRFLODVFTTLVDLKWPHTLLIFTMSFLCSWLLFANVWWLIAFAHGDLyaymekgitd
JS-10-665- JS-10-665- JS-10-665- JS-10-665-	1648 1638 1638	
S-10-665- IS-10-665- IS-10-665- IS-10-665- Consensus	1709 1689 1689 1689	ONIVGLMINAIMLGCIFMKTAQAHRRAETLIFSKHAVITLRHGRLCFMLRVGDLRKSMIIS
S-10-665- S-10-665- S-10-665- S-10-665- Consensus	1770 1750 1750 1750	ATIHWQVVRKTTSPEGEVVPLHQVDIPMENGVGGNGIFLVAPLIIYHVIDSNSPLYDLAPS

US-10-665. 1831 DLHHHQDLEIIVILEGVVETTGITTQARTSYLADEILWGQRFVPIVAEEDGRYSVDYSKFG

DLAHHQDLEIIVILEGVVETTGITTQARTSYLADEILWGQRFVPIVAEEDGRYSVDYSKFG NTIKVPTPLCTARQLDEDRS1ldaltlassrgplrkrsvavakakpkfsispdsls US-10-665- 1892 NTIKVPTPLCTARQLDEDRSLLDALTLASSRGPLRKRSVAVAKAKPKFSISPDSLS US-10-665- 1872 NIKVPTPLCTARQLDEDRSLLDALTLASSRGPLRAASVAVAKAKPKFSISPDSLS US-10-665- 1872 NTIKVPTPLCTARQLDEDRS US-10-665- 1872 NTIKVPTPLCTARQL 1611 1711 1925 1827 1825 Alignment score = 5263.00 1711 US-10-665- 1811 Scoring matrix: consensus consensus

WARN WHALE TUNG BINT